

# Species detectives track unseen evolution

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New species are evading detection using a foolproof disguise – their own unchanged appearance. Research published in the online open access journal, *BMC Evolutionary Biology*, suggests that the phenomenon of different animal species not being visually distinct despite other significant genetic differences is widespread in the animal kingdom.

DNA profiles and distinct mating groups are the only way to spot an evolutionary splinter group from their look-alike cousins, introducing uncertainty to biodiversity estimates globally.

Markus Pfenninger and Klaus Schwenk searched the Zoological Record database (1978-2006) to pinpoint reports of hidden (cryptic) species both biogeographically and taxonomically, and found 2207 examples. Pfenninger and Schwenk, who are from Germany based at J.W. Goethe-Universität in Frankfurt found evidence for cryptic species evenly spread among all major branches of the animal kingdom. They also found that cryptic species were just as likely to be found in all biogeographical regions.

The findings go against received wisdom that the insect or reptile branches of the animal kingdom are more likely to harbour cryptic species, and that these are more likely to be found in the tropics than in temperate regions. Zoologists should therefore consider factoring in a degree of cryptic diversity as a random error in all biodiversity assessments.

A cryptic species complex is a group of species that is reproductively

isolated from each other - but lacking conspicuous differences in outward appearance. Researchers using techniques such as polymerase chain reaction (PCR) and DNA sequencing have increasingly discovered - often unexpectedly - that similar-looking animals within a presumed species are in fact genetically divergent. As well as highlighting hidden biodiversity among creatures zoologists have already catalogued, the findings have implications for conservation efforts. Another possibility is that pathogens, parasites and invasive species disguised as their relatives may yet remain undetected, representing a potential human health threat.

Source: BioMed Central

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